

10/048197

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SEQUENCE LISTING

<110> Joelle THONNARD

<120> Novel Compounds

<130> BM45399

<150> 9918034.1

<151> 1999-07-30

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 336

<212> DNA

<213> Moraxella catarrhalis

<400> 1

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accatcatta agggcaagac caataagcaa gagattcta gtagatttg ttctgctgat	180
agcatctctt ttatgatagt ggtaataaaa tttggacata ccgccatact cgctccaaac	240
cgtatggcaag aaattttatc ccttataatt tctttctt gggtaaaacc atacagacca	300
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<210> 2

<211> 111

<212> PRT

<213> Moraxella catarrhalis

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Gln Asn Gln Gln Thr Ile Glu Gln Thr Ile Ile Lys Gly Lys Thr Asn	
35 40 45	
Lys Gln Glu Ile Ser Ser Arg Phe Gly Ser Ala Asp Ser Ile Ser Phe	
50 55 60	
Met Ile Val Val Ile Lys Phe Gly His Thr Ala Ile Leu Ala Pro Asn	
65 70 75 80	
Arg Trp Gln Glu Ile Leu Ser Leu Ile Ile Ser Phe Leu Trp Val Lys	
85 90 95	
Pro Tyr Arg Pro Lys Asn Leu Ser Phe Tyr Leu Thr Ala Lys Ala	
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<212> DNA

<213> Moraxella catarrhalis

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cctgtcggtc agcagattga tgacatttc caagcaccag ccatgcaagc aaatctacaa	180
aatggtatca agcagtccat tcttgatgcc gtgatgagcc aatgacgga tgcagacccc	240
aaccaacgcc tcgccataca aaataccatt ggtcagcagc tgaatacttt acaaattcacc	300
acccaaaatg ccacgaattt tgccgatagc tgtatggcgg atgtacatat aacggtaaac	360
ccccaaagatt tggcgaatgc agaatttgc tttgctcggt caggggtaac tttattacag	420
cgtgctagcc aagatcaagt ttagtttat aatggcacaa ttgtcgccaa acaaataact	480
tatcaaattgg tcaatggtaa tgtggatgt tatggcaaca atcataatgc cattttctg	540
attgccgata tttggcagc ttctacaagc agtttgcac aagtatccat acaatctgat	600
gttaccgcac gaccacaagg aattgagcga ctgcccagg caccaatagc tatgccccatca	660
aatcctcaag aagattctag tgtaacgacg tacattgaac aaaagccagc acctaacgca	720
caggtgtcat ctcgcccacg cagcggatgt tcttcaaata attcagcaca gacacccaca	780
caaaaactcgg tagggcaatc ttctgcagct ggtacgaccc ctcgtgtgga tcgtgatagt	840
caagccaaag ccaataccga gcgtaccacc gagcgttctg caaataagac atctcaagac	900
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<210> 4

<211> 328

<212> PRT

<213> Moraxella catarrhalis

<400> 4

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Asp Asp Glu Met Ala Val Ala Glu Pro Val Val Gln Gln Ile Asp Asp			
35	40	45	
Ile Cys Gln Ala Pro Ala Met Gln Ala Asn Leu Gln Asn Gly Ile Lys			
50	55	60	
Gln Ser Ile Leu Asp Ala Val Met Ser Gln Met Thr Asp Ala Asp Pro			
65	70	75	80
Asn Gln Arg Leu Ala Ile Gln Asn Thr Ile Gly Gln Gln Leu Asn Thr			
85	90	95	
Leu Gln Ile Thr Thr Gln Asn Ala Thr Asn Phe Ala Asp Ser Cys Met			
100	105	110	
Ala Asp Val His Ile Thr Val Asn Pro Gln Asp Leu Ala Asn Ala Glu			
115	120	125	
Phe Ala Phe Ala Arg Ser Gly Val Thr Leu Leu Gln Arg Ala Ser Gln			
130	135	140	
Asp Gln Val Glu Phe Tyr Asn Gly Thr Ile Val Ala Lys Gln Ile Thr			
145	150	155	160
Tyr Gln Met Val Asn Gly Asn Val Val Met Tyr Gly Asn Asn His Asn			
165	170	175	
Ala Ile Leu Leu Ile Ala Asp Ile Leu Ala Ala Ser Thr Ser Ser Leu			
180	185	190	
Pro Gln Val Ser Ile Gln Ser Asp Val Thr Ala Arg Pro Gln Ala Ile			
195	200	205	
Glu Arg Leu Pro Glu Ala Pro Ile Ala Met Pro Ser Asn Pro Gln Glu			

210 215 220
Asp Ser Ser Val Thr Thr Tyr Ile Glu Gln Lys Pro Ala Pro Asn Ala
225 230 235 240
Gln Val Ser Ser Arg Pro Arg Ser Glu Met Ser Ser Asn Asn Ser Ala
245 250 255
Gln Thr Pro Thr Gln Asn Ser Val Gly Gln Ser Ser Ala Ala Gly Ser
260 265 270
Thr Pro Arg Val Asp Arg Asp Ser Gln Ala Lys Ala Asn Thr Glu Arg
275 280 285
Thr Thr Glu Arg Ser Ala Asn Lys Thr Ser Gln Asp Leu Pro His Pro
290 295 300
Gln Pro Pro Thr Ala Asn Ala Ser Ser Asp Gly Lys Thr Ser Ile Ser
305 310 315 320
Ile Val Glu Ser Asn Glu Thr Tyr
325